

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/357,704

DATE: 03/29/2001
TIME: 16:09:38

Input Set : A:\242-024.txt
Output Set: N:\CRF3\03292001\I357704.raw

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3 <110> APPLICANT: Bander, Neil H.
5 <120> TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
7 <130> FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
9 <140> CURRENT APPLICATION NUMBER: US 09/357,704
10 <141> CURRENT FILING DATE: 1999-07-20
12 <150> PRIOR APPLICATION NUMBER: US 08/838,682
13 <151> PRIOR FILING DATE: 1997-04-09
15 <150> PRIOR APPLICATION NUMBER: US 60/016,976
16 <151> PRIOR FILING DATE: 1996-05-06
18 <150> PRIOR APPLICATION NUMBER: US 60/022,125
19 <151> PRIOR FILING DATE: 1996-07-18
21 <160> NUMBER OF SEQ ID NOS: 21
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 391
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus sp.
30 <400> SEQUENCE: 1
31 tctcctgtca ggaactgcag gtgtcctctc tgaggtccag ctgcaacagt ctggacctga 60
33 actggtgaag cctgggactt cagtgaggat atcctgcaag acttctggat acacattcac 120
35 tgaatatacc atacactggg tgaagcagag ccatggaaaag agccttgagt ggattggaaa 180
37 catcaatcct aacaatgggtg gtaccaccta caatcagaag ttcgaggaca aggccacatt 240
39 gactgtagac aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga 300
41 ttctgcagtc tattattgtg cagctggttg gaactttgac tactggggcc aaggcaccac 360
43 tctcacagtc tcctcagcca aaacgacacc c 391
46 <210> SEQ ID NO: 2
47 <211> LENGTH: 391
48 <212> TYPE: DNA
49 <213> ORGANISM: Mus sp.
51 <400> SEQUENCE: 2
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54 ccaaccagct gcacaataat agactgcaga atcctcagat gttaggctgc ggagctccat 120
56 gtaggctgta ctggaggact tgtctacagt caatgtggcc ttgtcctcga acttctgatt 180
58 gtaggtggtg caaccattgt taggattgat gtttccaatc cactcaaggc tctttccatg 240
60 gctctgcttc acccagtgta tggatatattc agtgaatgtg tatccagaag tcttcgagga 300
62 tatcctcact gaagtcccag gcttcaccag ttcaggtcca gactgttgca gctggacctc 360
64 agagaggaca cctgcagttc ctgacaggag a 391
67 <210> SEQ ID NO: 3
68 <211> LENGTH: 123
69 <212> TYPE: PRT
70 <213> ORGANISM: Mus sp.
72 <400> SEQUENCE: 3
74 Ser Pro Val Arg Asn Cys Arg Cys Pro Leu Gly Pro Ala Ala Thr Val
75 1 5 10 15
77 Trp Thr Thr Gly Glu Ala Trp Asp Phe Ser Glu Asp Ile Leu Gln Asp
78 20 25 30
80 Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro

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81          35          40          45
83 Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His
84          50          55          60
86 Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val
87 65          70          75          80
89 Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys
90          85          90          95
92 Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Gly Pro Arg His
93          100          105          110
95 His Ser His Ser Leu Leu Ser Gln Asn Asp Thr
96          115          120
98 <210> SEQ ID NO: 4
99 <211> LENGTH: 130
100 <212> TYPE: PRT
101 <213> ORGANISM: Mus sp.
103 <400> SEQUENCE: 4
105 Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln
106 1          5          10          15
108 Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys
109          20          25          30
111 Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys
112          35          40          45
114 Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
115          50          55          60
117 Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
118 65          70          75          80
120 Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
121          85          90          95
123 Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
124          100          105          110
126 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
127          115          120          125
129 Thr Pro
130          130
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 125
134 <212> TYPE: PRT
135 <213> ORGANISM: Mus sp.
137 <400> SEQUENCE: 5
139 Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn
140 1          5          10          15
142 Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
143          20          25          30
145 Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
146          35          40          45
148 Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
149          50          55          60
151 Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
152 65          70          75          80

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154 Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
155                               85                               90                               95
157 Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
158                               100                               105                               110
160 Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
161                               115                               120                               125
163 <210> SEQ ID NO: 6
164 <211> LENGTH: 345
165 <212> TYPE: DNA
166 <213> ORGANISM: Mus sp.
168 <400> SEQUENCE: 6
169 gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctgggacttc agtgaggata      60
171 tcctgcaaga ctctctggata cacattcact gaatatacca tacactgggt gaagcagagc      120
173 catggaaaga gccttgagtg gattggaaac atcaatccta acaatgggtg taccacctac      180
175 aatcagaagt tcgaggacaa ggccacattg actgtagaca agtcctccag tacagcctac      240
177 atggagctcc gcagcctaac atctgaggat tctgcagtct attattgtgc agctggttgg      300
179 aactttgact actggggcca aggcaccact ctcacagtct cctca                      345
182 <210> SEQ ID NO: 7
183 <211> LENGTH: 345
184 <212> TYPE: DNA
185 <213> ORGANISM: Mus sp.
187 <400> SEQUENCE: 7
188 tgaggagact gtgagagtgg tgccttggcc ccagtagtca aagttccaac cagctgcaca      60
190 ataatagact gcagaatcct cagatgttag gctgcggagc tccatgtagg ctgtactgga      120
192 ggacttgtct acagtcaatg tggccttgtc ctccaacttc tgattgtagg tggtagcacc      180
194 atgttagga ttgatgttcc caatccactc aaggctcttt ccatggctct gcttcacca      240
196 gtgtatggtt tattcagtga atgtgtatcc agaagctctg caggatatcc tcaatgaagt      300
198 cccaggcttc accagttcag gtccagactg ttgcagctgg acctc                      345
201 <210> SEQ ID NO: 8
202 <211> LENGTH: 115
203 <212> TYPE: PRT
204 <213> ORGANISM: Mus sp.
206 <400> SEQUENCE: 8
208 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
209 1                               5                               10                               15
211 Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
212                               20                               25                               30
214 Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
215                               35                               40                               45
217 Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
218                               50                               55                               60
220 Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
221 65                               70                               75                               80
223 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
224                               85                               90                               95
226 Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
227                               100                              105                              110
229 Val Ser Ser
230                               115

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232 <210> SEQ ID NO: 9
233 <211> LENGTH: 363
234 <212> TYPE: DNA
235 <213> ORGANISM: Mus sp.
237 <400> SEQUENCE: 9
238 ttatatggag ctgatgggaa cattgtaatg acccaatctc ccaaatccat gtccatgtca      60
240 gtaggagaga gggtcacctt gacctgcaag gccagtgaga atgtggttac ttatgtttcc      120
242 tggatatcaac agaaaccaga gcagtctcct aaactgctga tatacggggc atccaaccgg      180
244 tacactgggg tccccgatcg cttcacaggc agtggatctg caacagattt cactctgacc      240
246 atcagcagtg tgcaggctga agaccttgca gattatcact gtggacaggg ttacagctat      300
248 ccgtacacgt tcggaggggg gaccaagctg gaaataaaac gggctgatgc tgcaccaact      360
250 gta                                                                    363
253 <210> SEQ ID NO: 10
254 <211> LENGTH: 363
255 <212> TYPE: DNA
256 <213> ORGANISM: Mus sp.
258 <400> SEQUENCE: 10
259 tacagttggt gcagcatcag cccgttttat ttccagcttg gtccccctc cgaacgtgta      60
261 cggatagctg taaccctgtc cacagtgata atctgcaagg tcttcagcct gcacactgct      120
263 gatggtcaga gtgaaatctg ttgcagatcc actgcctgtg aagcgatcgg ggacccagc      180
265 gtaccgggtt gatgccccgt atatcagcag tttaggagac tgctctggtt tctgttgata      240
267 ccaggaaaca taagtaacca cattctcact ggccttgcaag gtcaaggtga ccctctctcc      300
269 tactgacatg gacatggatt tgggagattg ggtcattaca atgttcccat cagctccata      360
271 taa                                                                    363
274 <210> SEQ ID NO: 11
275 <211> LENGTH: 121
276 <212> TYPE: PRT
277 <213> ORGANISM: Mus sp.
279 <400> SEQUENCE: 11
281 Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser
282 1          5          10          15
284 Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser
285          20          25          30
287 Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln
288          35          40          45
290 Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val
291          50          55          60
293 Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
294 65          70          75          80
296 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
297          85          90          95
299 Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile
300          100         105         110
302 Lys Arg Ala Asp Ala Ala Pro Thr Val
303          115         120
305 <210> SEQ ID NO: 12
306 <211> LENGTH: 114
307 <212> TYPE: PRT
308 <213> ORGANISM: Mus sp.
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310 <400> SEQUENCE: 12

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312 Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
313 1 5 10 15
315 Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
316 20 25 30
318 Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
319 35 40 45
321 Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
322 50 55 60
324 Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
325 65 70 75 80
327 Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
328 85 90 95
330 Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
331 100 105 110

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333 Leu Tyr

336 <210> SEQ ID NO: 13

337 <211> LENGTH: 116

338 <212> TYPE: PRT

339 <213> ORGANISM: Mus sp.

341 <400> SEQUENCE: 13

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343 Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
344 1 5 10 15
346 Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
347 20 25 30
349 Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
350 35 40 45
352 Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
353 50 55 60
355 Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
356 65 70 75 80
358 Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
359 85 90 95
361 Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
362 100 105 110

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364 Cys Thr Asn Cys

365 115

367 <210> SEQ ID NO: 14

368 <211> LENGTH: 321

369 <212> TYPE: DNA

370 <213> ORGANISM: Mus sp.

372 <400> SEQUENCE: 14

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373 aacattgtaa tgaccgaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60
375 ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggatatca acagaaacca 120
377 gagcagtcctc ctaaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
379 cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
381 gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300
383 gggaccaagc tggaataaaa a 321

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386 <210> SEQ ID NO: 15

VERIFICATION SUMMARY

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